

Copyright (c) 1993 - 2000	Compugen Ltd.	
4 protein - protein search, using sw model		
run on:	July 19, 2002, 14:14:28 ; Search time 30.15 Seconds (without alignments) 1663.964 Million cell updates/sec	
Title:	US-09-808-885-1	
perfect score:	1467	
Sequence:	1 MKNSPOKIKKRDRRAKKQ RQKREEEPERIKRLEELLESKP 290	
Scoring table:	BLOSUM62	
	Gapop 10.0 , Gapext 0.5	
Scored:	562222	
Total number of hits satisfying chosen parameters:		
Minimum DB seq length: 0		
Maximum DB seq length: 2000000000		
Post-processing: Minimum Match 0%		
Maximum Match 100%		
Listing first 45 summaries		
Q9bhbm3 paramecium	17	265
Q45198 caenorhabdi	18	262
P91570 caenorhabdi	19	259
Q06166 plasmodium	20	258
Q9srd1 arabidopsis	21	257.5
Q9yvuo drosophila	22	256.5
Q9u0n1 drosophila	23	253
Q27529 caenorhabdi	24	251.5
Q96229 plasmodium	25	249.5
Q9vp3 drosophila	26	248.5
Q62235 caenorhabdi	27	248
Q17966 caenorhabdi	28	247.5
Q76719 caenorhabdi	29	245.5
Q9yt19 ateline her	30	244.5
Q9gtw3 plasmodium	31	244
Q9n435 caenorhabdi	32	242.5
Q9zu69 arabidopsis	33	237
P91257 caenorhabdi	34	236
Q9nd10 babesia big	35	235.5
Q61164 plasmodium	36	235
Q95xk7 caenorhabdi	37	234.5
Q9yzd9 drosophila	38	234.5
Q35788 ratius norv	39	232
Q9zlu2 borrelia bu	40	230
Q22944 caenorhabdi	41	227.5
Q50870 borrelia bu	42	226.5
Q17909 caenorhabdi	43	224.5
Q960c4 drosophila	44	224
Q9vb74 drosophila	45	224

ALIGNMENTS					
1:	sp_archaea:*				
2:	sp_bacteria:*				
3:	sp_fungi:*				
4:	sp_human:*				
5:	sp_invertebrate:*				
6:	sp_mammal:*				
7:	sp_mhc:*				
8:	sp_organelle:*				
9:	sp_genome:*				
10:	sp_plant:*				
11:	sp_rodent:*				
12:	sp_virus:*				
13:	sp_vertebrate:*				
14:	sp_unclassified:*				
15:	sp_rvirus:*				
16:	sp_bacteriopl:*				
17:	sp_archeapl:*				
RESULT 1					
P70488	P70488	PRELIMINARY;	PRT;	234 AA.	
AC P70488;	AC P70488;				
DT 01-FEB-1997 (TREMBLrel. 02, Created)	DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DE ANNEXIN V-BINDING PROTEIN (ABP-7) (FRAGMENT).				
OS Rattus norvegicus (Rat).	OC Mammalia; Eutheria; Rodentia; Muridae; Murinidae; Murinae; Rattus.				
NCBI_TaxID=10116;	OX NCBI_TaxID=10116;				
RN [1]	RN [1]				
SEQUENCE FROM N.A.					
RC STRAIN=MISTAR; TISSUE=BRAIN;	RC STRAIN=MISTAR; TISSUE=BRAIN;				
RX PubMed=96301899; Published=8667030;	RX PubMed=96301899; Published=8667030;				
RA Ohsawa K., Imai Y., Ito D., Kohsaka S.;	RA Ohsawa K., Imai Y., Ito D., Kohsaka S.;				
RT "Molecular cloning and characterization of annexin V-binding proteins with highly hydrophilic peptide structure.";	RT "Molecular cloning and characterization of annexin V-binding proteins with highly hydrophilic peptide structure.";				
RL J Neurochem 67:83-97(1996).	RL J Neurochem 67:83-97(1996).				
DR EMBL; D64061;	DR EMBL; D64061;				
FT BAA1J937.1; -.	FT BAA1J937.1; -.				
NON_TER 1	NON_TER 1				
SEQUENCE 234 AA;	SEQUENCE 234 AA;				
SQ 234 AA;	SQ 234 AA;				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
8 Query Match Length DB ID Description					
1 855 58.3 234 11 P70488 P70488 rattus norv					
2 792 54.0 655 13 Q9W6Q4 Q9W6Q4 gallus galli					
3 327 22.3 513 10 Q9IW95 Q9IW95 nicotiana t					
4 317.5 21.6 932 5 Q9VZP5 Q9VZP5 drosophila					
5 315 21.5 1144 5 Q9NH7 Q9NH7 drosophila					
6 314 21.4 390 5 Q18A01 Q18A01 caenorhabdi					
7 305 20.8 522 10 Q9FB5 Q9FB5 arabidopsis					
8 284.5 19.4 1224 10 Q9REI1 Q9REI1 arabidopsis					
9 283.5 19.3 2081 10 Q9JH98 Q9JH98 arabidopsis					
10 283 19.3 363 10 Q9YQ4 Q9YQ4 arabidopsis					
11 281 19.2 679 5 Q9XW8 Q9XW8					
12 279.5 19.1 260 10 Q9LGZ9 Q9LGZ9					
13 276.5 18.8 1280 10 Q9RD2 Q9RD2					
14 272 18.5 1166 10 Q9YP6 Q9YP6					
15 265.5 18.2 1791 13 Q9GSL1 Q9GSL1 fugu rubrip					
16 266 18.1 1192 5 Q96127 Q96127 plasmoidium					
17 266 18.1 1192 5 Q96127 Q96127 dasekitvaqkaekkerkrdeefaklrlkekelelgkkdosokesorkfee					

Page 2

OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
CC	Ephydriidae; Drosophilidae; Drosophila.		
NCBI_TaxID	7277		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY;		
RX	ADAMS M.D.; Celinker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.; Adams M.D.; Celinker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.; Gocayne J.D.; Harkness R.W.; Hoskins R.A.; Gocayne J.D.; Adams M.D.; Celinker S.E.; Richards S.; Ashburner M.; Henderson S.N.; Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.; Brandon R.C.; Rogers J.-H.C.; Blazier R.G.; Champé M.; Pfiffner B.D.; Wan K.H.; Doyle C.; Baxter E.G.; Heit G.; Nelson C.R.; Miklos G.L.G.; Abil J.F.; Agbayani A.; An H.-J.; Andrews-Pfannkoch C.; Baldwin D.; Ballew R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Basiley E.M.; Beeson K.Y.; Benos P.V.; Berman B.P.; Bhambhani D.; Bolshakov S.; Borovka D.; Btchian M.R.; Bouck J.; Brockstein P.; Brottier P.; Burts K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.; Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.; de Pablo B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.; Douson K.; Doup L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P.; Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferreira S.; Fleischmann W.; Fosler C.; Gabrilian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.; Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.; Harris N.L.; Harvey D.; Heiman T.J.; Hernandez J.R.; Houck J.; Houston K.A.; Houston K.A.; Howland T.J.; Wei M.H.; Ibeagwu C.; Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.; Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.; Lasko P.; Lei Y.; Levitus K.A.A.; Li J.; Li Z.; Liang Y.; Lin X.; Liu X.; Mattel B.; McIntosh T.C.; McLeod M.P.; McPhereson D.; Merklod G.; Millashina N.V.; Moberly C.; Morris J.; Mosherf A.; Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muzny D.M.; Nelson D.L.; Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Pacile J.M.; Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.; Reiner K.; Remington K.; Saunders R.D.C.; Scheeler P.; Shen H.; Shue B.C.; Silden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.; Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.; Svartkas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.; Wang Z.-Y.; Wasserman D.A.; Weinstock G.M.; Wessendorbach J.; Williams S.M.; Woodage T.; Wu D.; Yang S.; Yao Q.A.; Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhang G.; Zhao Q.; Zheng L.; Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.; RT "The genome sequence of Drosophila melanogaster."; RUEMPEL; AS003478; AAFA4774.1; -.		
RA	Li Y.; Levitus K.A.A.; Li J.; Li Z.; Liang Y.; Lin X.; Liu X.; Mattel B.; McIntosh T.C.; McLeod M.P.; McPhereson D.; Merklod G.; Millashina N.V.; Moberly C.; Morris J.; Mosherf A.; Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muzny D.M.; Nelson D.L.; Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Pacile J.M.; Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.; Reiner K.; Remington K.; Saunders R.D.C.; Scheeler P.; Shen H.; Shue B.C.; Silden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.; Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.; Svartkas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.; Wang Z.-Y.; Wasserman D.A.; Weinstock G.M.; Wessendorbach J.; Williams S.M.; Woodage T.; Wu D.; Yang S.; Yao Q.A.; Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhang G.; Zhao Q.; Zheng L.; Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.; RT "The genome sequence of Drosophila melanogaster."; RUEMPEL; AS003478; AAFA4774.1; -.		
LA	FlyBase; FBgn0026759; CIEF2; InterPro; IPRO00795; GTP_EFTU; InterPro; IPRO00151; GTP_EFTU_D2; Pfam; PF000009; GTP_EFTU; 1; DR Pfam; PF03144; GTP_EFTU_D2; 1; DR PRINTS; PR00315; BLONGTNTFCP; GTP-binding; Protein biosynthesis; KW GTP-binding; Protein binding; Protein biosynthesis; SEQUENCE 932 AA; 102828 MW; 3899c68FF38ED23F CRC64;		
QY	7 QKIKKRDRRAKQSF---DNDSEEDDKDSKSKTKAATPKVEMYSGDDDDFNKLKP 62		
DR	79 EEVVPAKGAKSKSAFELLMDDEQDEPAQSQESEKEVKKVVSK-----PQ 125		
DB	QY 63 KAKGKAOKSNKNGSEEDDKSKTKAATPKVEMYSGDDDDFNKLKP 112		
DR	126 KNEKGGKAKRK---GKDDDELDKVLAELQAEYAGEAPATTVVSPPEELAFSKKK 183		
QY	113 GQKKQNKPGNII -ESGNEDDDASFKTVQKKAEEKKERKDEEKAKLRKKEK 170		
DR	184 NKQQAQAAVAENAGEDASDDEEGGSTVKSAAQKKKEKERO -KREAAA -K 234		
QY	171 ELEETGKRDQSISKORESQRKFEEETVKSVTDTGVIASEEEAETPTAAEDNEGDKKK 230		
Query Match	21.6%; Score 317.5; DB 5; Length 932;		
Best Local Similarity	30.9%; Pred. No. 6.9e-10;		
Matches	92; Conservative 61; Mismatches 88; Indels 57; Gaps 11;		
QY	7 QKIKKRDRRAKQSF---DNDSEEDDKDSKSKTKAATPKVEMYSGDDDDFNKLKP 62		
DR	79 EEVVPAKGAKSKSAFELLMDDEQDEPAQSQESEKEVKKVVSK-----PQ 125		
DB	QY 63 KAKGKAOKSNKNGSEEDDKSKTKAATPKVEMYSGDDDDFNKLKP 112		
DR	126 KNEKGGKAKRK---GKDDDELDKVLAELQAEYAGEAPATTVVSPPEELAFSKKK 183		
QY	113 GQKKQNKPGNII -ESGNEDDDASFKTVQKKAEEKKERKDEEKAKLRKKEK 170		
DR	184 NKQQAQAAVAENAGEDASDDEEGGSTVKSAAQKKKEKERO -KREAAA -K 234		
QY	171 ELEETGKRDQSISKORESQRKFEEETVKSVTDTGVIASEEEAETPTAAEDNEGDKKK 230		
Query Match	21.5%; Score 315; DB 5; Length 1144;		
Best Local Similarity	30.3%; Pred. No. 1.1e-09;		
Matches	92; Conservative 61; Mismatches 97; Indels 54; Gaps 10;		
QY	11 KRKDRRAKQKQSPEDDNDSSELEKDKSKKTAATPKVEMYSGDDDD-----56		
DR	60 KKLNVKRGKAGRNDSDDEEVYPAKGRASKSAFELLMDDEQDEPAQESSEEEKV 119		
DR	57 FNKLPPKKRKGACKNSKWKDGSEEDDKSKTKERSRINTSGSGS-----DESD 106		
DR	120 VVSKPQNEKKGKAKRK---GKDDDELDKVLAELQAEYAGEAAPATTVVSPPEELADE 177		
QY	107 FLSRKGGDKKNQNKPGNII -ESGNEDDDASFKTVQKKAEEKKERKDEEKAKL 164		
DR	178 FSKKKKKQAKGAAVANAGEDBEASDEEGGSTVKSAAQKKKEKERO -KREAAA - 233		
QY	165 RKLKEKELETGKQDKSQKOKSQRKFEEETVKSVTDTGVIASEEEAETPTAAEDONE 224		
DR	234 -----KQAAATEEKPKPKPAP ---EVPAEAE -----E-EKKS 272		
DR	225 GDKKKKDKKKKKGEKEKEKE -KKKGPKSKATVKAMQELAKLKKEEEQKREBEEIKRL 283		
DR	273 SKNKKGKDKKAPEEEKKDAKKGMASMYAAMQELRKREEEEELREEAERIRLE 332		
QY	284 EEL E 287		
DR	333 DERE 336		
RESULT	6		
ID	Q18401 PRELIMINARY;		
AC	Q18401; 01; Created)		

DR	Pfam: PF03144; GTP_EFTU_D2; 2.	Query Match Score 19.3%; Best Local Similarity 27.4%; Matches 1;	Match 283; Local Similarity 9.4%; Pred. No. 9-e-08; Conservative 60; Mismatches 98; Indels 67; Gaps 11;
DR	PRINTS: PR0015; BLONGATNFCF.		
DR	PROSITE: PS00358; RIBOSOMAL_L5; UNKNOWN_1.		
KW	GTP-binding; Initiation factor; Protein biosynthesis.		
SEQUENCE	1224 AA; 13501 MW; 6C25811EB0B7002 CRC64;		
Query Match Score 19.4%; Best Local Similarity 25.6%; Matches 111; Conservative 56; Mismatches 109; Indels 157; Gaps 18;	Query Match Score 19.3%; Best Local Similarity 27.4%; Matches 85; Conservative 60; Mismatches 98; Indels 67; Gaps 11;		
QY . 1 MKRNSPQRKIKRKDRR-----AKQSF--DDNDSEEELEDKSKSKTAKPK--V 4.5	QY 1 MKRNSPQRKIKRKDRR-----AKQSF--DDNDSEEELEDKSKSKTAKPK--V 4.5	QY 1 MKRNSPQRKIKRKDRR-----AKQSF--DDNDSEEELEDKSKSKTAKPK--V 4.5	QY 1 MKRNSPQRKIKRKDRR-----AKQSF--DDNDSEEELEDKSKSKTAKPK--V 4.5
DB 11 MGRRKPSSRGKDEQPAAASSLVGAESKKAVQSDDEDKYSINTEEEKVVTGKKSNK 70	DB 11 MGRRKPSSRGKDEQPAAASSLVGAESKKAVQSDDEDKYSINTEEEKVVTGKKSNK 70	DB 906 VQSGSGEVSYKVKEDEKKRNKGKRRKKKKKEKSNSNMKKKEEDKE 965	DB 906 VQSGSGEVSYKVKEDEKKRNKGKRRKKKKKEKSNSNMKKKEEDKE 965
QY 46 EMYGSDDDDDFIQL-----PKAAGKQAKQSNKWK----DGSEEDDNKKIKERSR 93	QY 46 EMYGSDDDDDFIQL-----PKAAGKQAKQSNKWK----DGSEEDDNKKIKERSR 93	QY 57 F--NKLPKKAKGKAQSKNSNKKWDSEEDDKSKTAKPKVNTTNTSKQGK 114	QY 57 F--NKLPKKAKGKAQSKNSNKKWDSEEDDKSKTAKPKVNTTNTSKQGK 114
D 71 K7TQKHDDDDTFEAEPENGFYGKQKSKKGKRGGSVSFALLSGKEETDDNE-----1.22	D 71 K7TQKHDDDDTFEAEPENGFYGKQKSKKGKRGGSVSFALLSGKEETDDNE-----1.22	DB 966 YVNEL-----KKQEDKK-----ETTSENSKLKEENKDNEKEEDSDS---ASKRE 1011	DB 966 YVNEL-----KKQEDKK-----ETTSENSKLKEENKDNEKEEDSDS---ASKRE 1011
QY 94 INSSGESDDESDFEFLQSRKGQKK--NQNNKPGDNIES-----AS 1.36	QY 94 INSSGESDDESDFEFLQSRKGQKK--NQNNKPGDNIES-----AS 1.36	QY 115 KKQKQKPGNTIESGNEDDASFATKITYAQKKAERKERKDEEAKLRLKEELE 174	QY 115 KKQKQKPGNTIESGNEDDASFATKITYAQKKAERKERKDEEAKLRLKEELE 174
DB 123 -----SNCDKDDPEPVISTGKKNASNNGKKGAVASA DALGGDKDDEVDGEEQVSPLIT 1.77	DB 123 -----SNCDKDDPEPVISTGKKNASNNGKKGAVASA DALGGDKDDEVDGEEQVSPLIT 1.77	DB 1012 KKEYEK-----KSKTVEAEKKKKSDQKKBREEKDSBERKSKEKEES 1055	DB 1012 KKEYEK-----KSKTVEAEKKKKSDQKKBREEKDSBERKSKEKEES 1055
QY 137 EKIKTVQAKKAERK-----ERERKKRDEE-----1.60	QY 137 EKIKTVQAKKAERK-----ERERKKRDEE-----1.60	QY 175 TGKDDOSKOKESQRKFEEBTVKSKVYTDGVIPASEEKAETPFAAEDNEGDKKKKKK 234	QY 175 TGKDDOSKOKESQRKFEEBTVKSKVYTDGVIPASEEKAETPFAAEDNEGDKKKKKK 234
DB 178 FSGKTRSSSKSSKTTNKVALDDEEGTMGEESLEITFGKKKGSTIVLASLGDDSYADE 237	DB 178 FSGKTRSSSKSSKTTNKVALDDEEGTMGEESLEITFGKKKGSTIVLASLGDDSYADE 237	DB 1056 RDJAKKKEEEETKEEENHKS-----KKEDKE-----HENKSMKKEEDKE 1101	DB 1056 RDJAKKKEEEETKEEENHKS-----KKEDKE-----HENKSMKKEEDKE 1101
QY 161 - KAKLRALKKEEELETKKDKSOKESQ--RKFEETVKSPTVDTGVIPSEEERAKET- 215	QY 161 - KAKLRALKKEEELETKKDKSOKESQ--RKFEETVKSPTVDTGVIPSEEERAKET- 215	QY 235 KKGEKEKEKEK-----KKGPSKATVKAMOEALAKLKEEEEROKREEEE 278	QY 235 KKGEKEKEKEK-----KKGPSKATVKAMOEALAKLKEEEEROKREEEE 278
DB 238 TSGAKTPDTKSVIEYGKIKRKKNKVNVALDDEEGTMGEESLEITFGKKKGSTIVLASLGDDSYADE 297	DB 238 TSGAKTPDTKSVIEYGKIKRKKNKVNVALDDEEGTMGEESLEITFGKKKGSTIVLASLGDDSYADE 297	DB 1102 KKHHEESSRSRKKEEDDKMKELEDQNSUKKKEDKNEKKKSQHVLYKVKVESDKKEKEKKEENEE 1161	DB 1102 KKHHEESSRSRKKEEDDKMKELEDQNSUKKKEDKNEKKKSQHVLYKVKVESDKKEKEKKEENEE 1161
QY 216 -----PTAAEDDNEGDK-----KKDKKKKKGE-----K 239	QY 216 -----PTAAEDDNEGDK-----KKDKKKKKGE-----K 239	QY 279 RIKRLEELLES 288	QY 279 RIKRLEELLES 288
DB 298 PEYEKVQAQGPVAPVENAGEEGEKEKETVETAAKKKKKKDKKEKEKAATSSYEAK 357	DB 298 PEYEKVQAQGPVAPVENAGEEGEKEKETVETAAKKKKKKDKKEKEKAATSSYEAK 357	DB 1162 K-SETKEIES 1170	DB 1162 K-SETKEIES 1170
QY 240 EKEKE-----KKKGPSKAT-----VKAMOEALAKKEEEEROKRBEERT---- 280	QY 240 EKEKE-----KKKGPSKAT-----VKAMOEALAKKEEEEROKRBEERT---- 280	Q93VQ4 PRELIMINARY; PRIT; 363 AA.	Q93VQ4 PRELIMINARY; PRIT; 363 AA.
DB 358 EKEQEESVTEPLQPKKDAKGKAEEKKKIPKHYREMQEALARQEAEERKKKEEEKLKRKE 417	DB 358 EKEQEESVTEPLQPKKDAKGKAEEKKKIPKHYREMQEALARQEAEERKKKEEEKLKRKE 417	AC Q93VQ4; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	AC Q93VQ4; DT 01-DEC-2001 (TREMBLrel. 19, Created) DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
QY 281 ---KRLBELESK 289	QY 281 ---KRLBELESK 289	DE HYPOTHETICAL 42.4 KDa PROTEIN (FRAGMENT).	DE HYPOTHETICAL 42.4 KDa PROTEIN (FRAGMENT).
DB 418 EEERRQBEELEAQ 430	DB 418 EEERRQBEELEAQ 430	OS Arabidopsis thaliana (Mouse-ear cress). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; OC eurosids II; Brassicales; Brassicaceae; Arabidopsis; OX NCBI_TaxID=3702; RN [1]	OS Arabidopsis thaliana (Mouse-ear cress). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; OC eurosids II; Brassicales; Brassicaceae; Arabidopsis; OX NCBI_TaxID=3702; RN [1]
QY 28 PRELIMINARY; PRIT; 2081 AA.	QY 28 PRELIMINARY; PRIT; 2081 AA.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
AC Q9LH98; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	AC Q9LH98; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	RA Nguyen M., Karlin Neumann G., Southwick A., Lam B., Miranda M., PA Lin C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamaya A., Kawai J., RA Kim C., Lin J., Liu X., Narusaka M., Pham P.K., Salzano H., RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., RA Ecker J., Theologis A., Davis R.W.; RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL; AY059831; AAU24313.1; -. KW Hypothetical protein. FT NON_TER 363 SQ SEQUENCE 363 AA; MW DB5A4D487A4936 CRC64;	RA Nguyen M., Karlin Neumann G., Southwick A., Lam B., Miranda M., PA Lin C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamaya A., Kawai J., RA Kim C., Lin J., Liu X., Narusaka M., Pham P.K., Salzano H., RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., RA Ecker J., Theologis A., Davis R.W.; RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL; AY059831; AAU24313.1; -. KW Hypothetical protein. FT NON_TER 363 SQ SEQUENCE 363 AA; MW DB5A4D487A4936 CRC64;
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
STRAIN=COLUMBIA; RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.	STRAIN=COLUMBIA; RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.	QY 1 MKRNSPQRKIKRKDRR-----DSEEEKDSSKPKAKPVYEMYSSD 52	QY 1 MKRNSPQRKIKRKDRR-----DSEEEKDSSKPKAKPVYEMYSSD 52
[2]	[2]	DB 37 VKAKSIEVKAKDEESSGSKKDKKKQVSKKHEEKGK 96	DB 37 VKAKSIEVKAKDEESSGSKKDKKKQVSKKHEEKGK 96
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	QY 53 DD-----EDENKLPKKAK-----GKAQKSNKWDGSEEDEDNSKKKE 90	QY 53 DD-----EDENKLPKKAK-----GKAQKSNKWDGSEEDEDNSKKKE 90
STRAIN=COLUMBIA; MEDLINE=20363099; PubMed=10907853;	STRAIN=COLUMBIA; MEDLINE=20363099; PubMed=10907853;	DB 97 GDLEVKESEDVYKEHEKHKGGKKEKKHEELEEEKGK 156	DB 97 GDLEVKESEDVYKEHEKHKGGKKEKKHEELEEEKGK 156
"Structural analysis of Arabidopsis thaliana chromosome 3 II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, RT TAC and BAC clones"; DNA Res. 7:217-221(2000); EMBL; AP002057; BAB03174.1; SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFFF29 CRC64;	"Structural analysis of Arabidopsis thaliana chromosome 3 II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, RT TAC and BAC clones"; DNA Res. 7:217-221(2000); EMBL; AP002057; BAB03174.1; SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFFF29 CRC64;	QY 91 RSRINSSGSGDESDEFLOSSRKGGKKNQKNKGPNIESNDDASFMKIKTVAQKKAKRK 150	QY 91 RSRINSSGSGDESDEFLOSSRKGGKKNQKNKGPNIESNDDASFMKIKTVAQKKAKRK 150

RN [1]	SEQUENCE FROM N.A.	RA Fedderspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RP	STRAIN=CV. COLUMBIA;	RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RC		RA Gonzalez A., Kremenevskaya I., Kim C., Lenz C., Li J., Liu S.,
RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,	RA Larios S., Schwartz J., Shinn P., Toriumi M., Vysotskaya V.S.,
RA	Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,	RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RA	Barnstead M.E., Bowman C.L., White O., Nieman W.C., Fraser C.M.;	Submitted (MAY 1999) to the EMBL/GenBank/DBJ databases.
RA	"Arabidopsis thaliana chromosome 1 BAC F28O16 genomic sequence."	CC "1-SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE.
RL	Submitted (OCT 2000) to the EMBL/GenBank/DBJ databases.	DR EMBL; AC010718; AAD30599.1; -.
DR	EMBL; AC010718; AAF0442.1; -.	DR HSSP; Q58083; IHV8.
DR	InterPro: IPR000795; GTP_EFTU.	DR InterPro; IPR001410; DEAD.
DR	InterPro: IPR004161; GTP_EFTU_D2.	DR InterPro; IPR006629; DEAD_ATP_helicase.
DR	InterPro: IPR000178; IF2.	DR InterPro; IPR001650; Helicase_C.
Pfam	GTP_EFTU; 1.	PFAM; PF00270; DEAD; 1.
DR	Pfam; PF03144; GTP_EFTU_D2; 1.	DR Pfam; PF00271; helicase_C; 1.
DR	PRINTS; PRO0315; ELONGATNPCT.	SMART; SM00490; HELIC_C; 1.
KW	GTP-binding; Initiation factor; Protein biosynthesis.	PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
SO	SEQUENCE_1280 AA; 140708 MW; BC1A2BF7A5839D0C CRC64;	ATP-binding; Helicase; RNA-binding.
SO	SEQUENCE_1166 AA; 133033 MW; 597BD171F02666B5 CRC64;	SEQUENCE_1166 AA; 133033 MW; 597BD171F02666B5 CRC64;
Query Match	Score 26.5; DB 10; Length 1280;	
Best Local Similarity	26.04; Pred. No. 1.4e-07;	
Matches	111; Conservative 59; Mismatches 100; Indels 157; Gaps 19;	
Qy	18 KKQSFDNDSELEDKDSKSKKTARPKVNEYSG-----SDDDDF-----57	Query Match 18.5%; Score 272; DB 10; Length 1166;
Db	30 KGAQIDDYE5IGTELSEESKEEVKVVITGKKGKGNKGQTQDDDDFSDKVSA 89	Best Local Similarity 25.5%; Pred. No. 2.3e-07;
Qy	58 ---NKLP-----KKAKGKA-----QNSNKWKDGSEEDEDKDSKSKKTARPKVNEYSG-----SDDDDF-----84	Matches 77; Conservative 98; Mismatches 75; Indels 52; Gaps 11;
Db	90 GVKDVPEIAFGKRSKRGKGGSVSALLDEDKEDNESGKDKDDEPVTSFTGKKA 149	Qy 10 KKRKDRAKKSFDDNDSEELDKDSKSKKTARPKVNEYSGSSDDDFNKLPKKAGKQA 69
Qy	85 SKIKE-----RSRINNSGEGDESDEFQ-----SRKGQKKNNQKN-----120	Db 24 KSRRDRSNERSREKKDKGSEKREKDRKVR-----KSDDSEDDYDRDDEEEK--73
Db	150 SKGKGGNSPAASAFALGSDDDOTEVEHDEEEESPTIFSGKSKSSKNTNSFT 209	Qy 70 KSNKWDGSEEDEDNSKKIKERSRINNSGEGDESDE-----FLQSRKGQKKNNQKPGP 124
Qy	121 -----KPGNTEGND-----DDASFKIRTVAOKAERK-----RERKDRDEEK 161	Db 74 RKEKERERRRRDKDYSKRSRERKSSDDEEDDKRNEKERGREHERDR-GK 132
Db	210 ADLLDEEGTDAISNRDDENTIDEESPEVTFSGKSKKKGGSYGVDSVADETK 269	Qy 125 NIESGNEDDDAFSKIKTVAQKAERKERERKDRDEEAKLKRKELETFGKKDOQKQ 184
Qy	162 AKLRKKEKEPLERGR-KDOSKQKESQRKEETVSKVTVDTGVIPAS-----EE 211	Db 133 DRKDRREERERDK-BREEREDRERREREREKVEREREREDGERREERER 191
Db	270 TS---DTKVNVEVTGSKKKKKNNNSGTVQEEDLDKLLAALGETPAABEPASPTPVEE 327	Qy 185 ESQRKFEEETVSKVTVDTGVIPASEEKAEPTAAEDNEQQ-----KEKEKE 244
Qy	212 KAETP-----TAAEDNEGD-----KKKKDKKKKG-----KEKEKE 245	Db 192 GSRRRNRRERSRE-----VGNEE-----SDDDVKRDLKR-RRKGERERKER 233
Db	328 KAQPQEVAPENAGKEGEETAAAKKKKKKEKEKEKAAAATSSYKEKEQEE 387	Qy 245 EKKKG-----PSKAVTKAMEALAKLKEEE----RKRREEEE-----RKRLEBLE 287
Qy	246 -----KKKGPSKAT-----VKAMOEAALAKLKEEEPRQKREEEET-----KR 282	Db 234 EKSVGRSSRHEDSPKRSKVEDNGEKEKKTREEELEDQKLDEEVKRRRVQEWQLK 293
Db	388 SYTEPLQPKKKDAKGKAEEAKIPKPVHREMQUEALARQEAEERKKKEEEERRR 447	RESULT 15
Qy	283 LEELSK 289	Q9DGL1 PRELIMINARY; PRT; 791 AA.
Db	448 QEELAQ 454	ID Q9DGL1 AC Q9DGL1; DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
RESULT 14		DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
Q9SYP6	PRELIMINARY; PRT; 1166 AA.	DE RETINTIS PIGMENTOSA CTIASE REGULATOR-LIKE PROTEIN (FRAGMENT).
AC		OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
DT	01-MAY-2000 (TREMBLrel. 13, Created)	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	OC Acanthomorpha; Acanthopterygii; Tetraodontiformes;
DE	F9H16_1.0 PROTEIN	OC Tetraodontidae; Takifugu.
GN	F9H16_1.0	OX NCBI_TaxID=31033;
OS	Arabidopsis thaliana (Mouse-ear cress).	RN [1] J. Sequence FROM N.A.
OC	Eukaryota; Viridiplantae; Streptophytina; Tracheophyta; Rosidae;	RA Vervoort R., Lennon A., Bird A.C., Tulloch B., Axton R., Miano M.G.,
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	RA Meitinger T., Ciccodicola A., Wright A.P.;
OC	eurosidia II; Brassicaceae; Arabidopsis.	RT "Mutational hot spot within a new PCR exon in x-linked retinitis pigmentosa.";
RN	[1] SEQUENCE FROM N.A.	RL Nat. Genet. 0:0-0(2000); AF286475; AAG0054.1; -.
RP	SEQUENCE FROM N.A.	DR EMBL; AF286475; AAG0054.1; -.
RC	STRAIN=CV. COLUMBIA;	FT NON_TER 1 1

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SQ  SEQUENCE   791 AA;   89672 MW;   DA40AFFA99E3B39 CRC64;
Query Match 18.2%; Score 267.5; DB 1.3; Length 791;
Best Local Similarity 24.1%; Pred. No. 2.9e-07;
Matches 70; Conservative 84; Mismatches 118; Indels 19; Gaps 6;
Qy  14 DRRAKKOSFDDNDEEL----EDKDSKS --KKTAKPVYMSGSSDDDFNKLPKKA 64
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Db  436 ERKKASESEEEEEEADSLSEEEDSKSDAEEAESAESET--GEAAEEEOSSTEKEGES 494
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Qy  65 KCGAQKSNKNGDSEEDEDNSRKIKERSRINSSEGSDESFQGS--RKGQQKNQKNKP 122
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Db  495 NEEQSSTEEKSNEEEEOSSTEKEESNEEEEOSSTEKEESNEEEEOSSTEKEESNEEEQSS 554
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Qy  123 GPNIESNEDDODASFKIITVAQQKAASKERERKKRREEEKAKLRKLUKEKEELETGKDKQSK 182
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Db  555 TEKEEEENEEOOSSTEKE--ESNEEEEEESEEESEEESEEESEEESEEESEEEDEEE 611
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Qy  183 QKESQRKFEEETVKSKVTVDGVIPASEEKAKTPAAEDDNGDKKKDKKKK---GE 338
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Db  612 EEESEEQNQEAEAEEDGEIDVQEEEEEETKEEDEEEETKEEDEEEETDRVEE 671
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Qy  239 KEEKEKEKKKGPSKATVKAMQALAKLKEERQKREEEERIKRLELESK 289
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||
Db  672 EPEAEEEEEPEBESNSEDEEDSGEEEDFSDEEDESESSEEEGE 722
      :|: :: :||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||: |: ||

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Search completed: July 19, 2002 14:18:09
Job time: 221 sec